OFFICIAL

AMENDMENTS TO THE CLAIMS

1. **(Currently amended):** A method for estimating the precision of measurements taken from an array, comprising:

    (a)   identifying a set of low-level data measurements;

    (b)   estimating a standard deviation, σ_ε of an additive error component, ε ;

    (c)   estimating a background parameter, α ;

    (d)   identifying a set of replicated high-level data measurements;

    (e)   estimating a standard deviation, σ_η , <u>of a proportional error component, η </u>from the standard deviation of the logarithm of the replicated high-level data set;

    (f)   measuring a signal, y, wherein said signal indicates an amount of a biological molecule; and

    (g)   estimating a variance of the measured signal as

$$\underline{Var\{y\} = \mu^2 e^{\sigma_\eta^2}\left(e^{\sigma_\eta^2} - 1\right) + \sigma_\varepsilon^2}$$

<u>wherein μ is the amount of the biological molecule and</u>

$$\underline{y = \alpha + \mu e^\eta + \varepsilon}$$

<u>and wherein each model quantity is replaced by an estimate thereof.</u>

~~$\hat{Var}(\hat{\mu}) = \hat{\sigma}_\varepsilon^2 + \hat{\mu}^2 e^{\hat{\sigma}_\eta^2}\left(e^{\hat{\sigma}_\eta^2} - 1\right),$ where $\hat{\mu}^2 = (y - \alpha)^2$~~

2. **(Original):** The method of claim 1, wherein said identifying step (a) comprises the use of a thresholding algorithm to establish a cutoff, and the set of low-level data consists of those data with values less than the cutoff.

3. **(Currently amended):** The method of claim 2, wherein the thresholding algorithm comprises the steps of:

    (a)   identifying A_N, an initial set of low-level data measurements consisting of q percent of the total number of data points having the lowest measurement values, $A_N = \{x_1, x_2, \ldots, x_{no}\}$;

    (b)   calculating a mean and a standard deviation of the initial set;

(c)   calculating a cutoff point, u_N = mean plus <u>($c \times$ the standard deviation)</u> ~~$c \times$ the standard deviation~~, wherein $2 \leq c \leq 3$;

(d)   defining a new set, $A_{N+1} = \{x_j < u_N\}$;

(e)   calculating a mean and standard deviation of the new set; and

(f)   repeating steps (c) and (d) using the mean and standard deviation of the new set until the algorithm converges.

4. (**Currently amended**):   The method of claim 2, wherein the thresholding algorithm comprises the steps of:

(a)   identifying A_N, an initial set, of low-level data consisting of q percent of the total number of data points having the lowest measurement values, $A_N = \{x_1, x_2, \ldots, x_{no}\}$;

(b)   calculating a median of the initial set, $m_o = \text{median} \left\{x_j\right\}_{j=1}^{n_o}$ and a median of the absolute deviations about the median, $MAD_0 = \text{median} \left\{\left|x_j - m_o\right|\right\}_{j=1}^{n_o}$;

(c)   calculating a cutoff point, $u_0 = MAD_0 + $ <u>($c \times s_0$)</u> ~~$c \times s_0$~~, wherein $s_o = MAD_0/0.675$ and $2 \leq c \leq 3$;

(d)   defining a new set, $A_{N+1} = \{x_j < u_N\}$;

(e)   calculating a median and a median of the absolute deviations about the median of the new set; and

(f)   repeating steps (c) and (d) using the median and the median of the absolute deviations about the median of the new set until the algorithm converges.

5. (**Original**): The method of claim 2, wherein the mean of the low-level data measurements is used as the estimate of the background parameter, α.

6. (**Original**): The method of claim 1, wherein the standard deviation of the low-level data measurements is used as the estimate of the parameter σ_ε.

7. (**Original**): The method of claim 1, wherein, a mean of negative control data is used as the estimate of the background parameter, α.

8. (**Original**): The method of claim 1, wherein the biological molecule is a nucleic acid.

9. (**Original**): The method of claim 8, wherein the nucleic acid is mRNA.

10. (**Original**):   The method of claim 8, wherein the biological molecule is DNA.

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11. **(Original)**:   The method of claim 10, wherein the DNA is cDNA.

12. **(Original)**:   The method of claim 10, wherein the DNA is genomic.

13. **(Withdrawn)**:   The method of claim 1, wherein the biological molecule is a

protein.

14. **(Withdrawn)**:   The method of claim 1, wherein the biological molecule is a lipid.

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